

## SEQUENCE LISTING

<110> Kharbanda, Surrender  
Kufe, Donald

<120> Modulation of Interaction of MUC1 with MUC1 Ligands

<130> ILEX:094WO

<140> Unknown

<141> 2004-10-21

<150> 60/514,198

<151> 2003-10-24

<150> 60/519,822

<151> 2003-11-12

<160> 71

<170> PatentIn version 3.3

<210> 1

<211> 164

<212> PRT

<213> Homo sapiens

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Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly  
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Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala  
35 40 45

Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Phe Asn  
50 55 60

Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg  
65 70 75 80

Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu  
85 90 95

Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu  
100 105 110

Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Met Glu Thr  
115 120 125

Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr  
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly  
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser  
 35 40 45

Thr Glu Lys Asn Ala Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp  
 50 55 60

Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile

Met	Thr	Pro	Gly	Thr	Gln	Ser	Pro	Phe	Phe	Leu	Leu	Leu	Leu	Leu	Thr
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Val	Leu	Thr	Val	Val	Thr	Gly	Ser	Gly	His	Ala	Ser	Ser	Thr	Pro	Gly
			20					25					30		

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser  
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 Thr Glu Lys Asn Ala Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser  
       50                                  55                                  60  
  
 Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser  
       65                                  70                                  75                                  80  
  
 Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu  
                                   85                                  90                                  95  
  
 Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe  
                                   100                                  105                                  110  
  
 Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly  
                                   115                                  120                                  125  
  
 Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr  
       130                                  135                                  140  
  
 Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser  
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 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Thr  
 35 40 45

Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln  
 50 55 60

Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg  
 65 70 75 80

Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr  
 85 90 95

Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu  
 100 105 110

Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp  
 115 120 125

Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly  
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 ccaggatctg tggtggtaca attgactctg gccttcgag aaggtaccat caatgtccac 300  
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly  
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser  
 35 40 45

Thr Glu Lys Asn Ala Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg  
 50 55 60

Glu Thr Phe Leu Lys Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu  
 65 70 75 80

Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe  
 85 90 95

Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser  
 100 105 110

Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly  
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Ala Gly  
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cagagaagtt cagtgccag ctctactgag aagaatgcta tcccagcacc gactactacc 180

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gccttccgag aagggtaccat caatgtccac gacatggaga cacagttcaa tcagtataaa 300

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Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly  
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Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val  
 35 40 45

Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val  
 50 55 60

Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn  
 65 70 75 80

Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser  
 85 90 95

Ala Gln Ser Gly Ala Gly  
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<210> 13

<211> 375  
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<400> 13

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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly  
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser  
 35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His  
 50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu  
 65 70 75 80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln  
 85 90 95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr  
 100 105 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro  
 115 120 125

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr  
 130 135 140

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser  
 145 150 155 160

Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val His  
 165 170 175

Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu  
 180 185 190

Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys  
 195 200 205

Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr Thr  
 210 215 220



Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser Thr His His Ser  
225 230 235 240

Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln Leu  
245 250 255

Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn Leu  
260 265 270

Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu  
275 280 285

Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly  
290 295 300

Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val  
305 310 315 320

Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp  
325 330 335

Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr  
340 345 350

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Ser Ala Gln Ser Gly Ala Gly  
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gtcccagtca ccaggccagc cctggggtcc accaccccg cagcccacga tgtcacctca 360  
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 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser  
 35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His  
 50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu  
 65 70 75 80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln  
 85 90 95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr  
 100 105 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Asn Arg Pro

115					120					125					
Ala	Leu	Gly	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser	Ala	Ser
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Ala	Arg	Ala	Thr	Thr	Thr	Pro	Ala	Ser	Lys	Ser	Thr	Pro	Phe	Ser	Ile
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Pro	Ser	His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His	Ser	Thr
			180					185					190		
Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His	Ser	Thr	Val	Pro	Pro	Leu	Thr
		195					200					205			
Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val	Ser	Phe
	210					215					220				
Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln	Phe	Asn	Ser	Ser	Leu
225					230					235					240
Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln	Glu	Leu	Gln	Arg	Asp	Ile	Ser
				245					250					255	
Glu	Met	Phe	Leu	Gln	Ile	Tyr	Lys	Gln	Gly	Gly	Phe	Leu	Gly	Leu	Ser
			260					265					270		
Asn	Ile	Lys	Phe	Arg	Pro	Gly	Ser	Val	Val	Val	Gln	Leu	Thr	Leu	Ala
		275					280					285			
Phe	Arg	Glu	Gly	Thr	Ile	Asn	Val	His	Asp	Val	Glu	Thr	Gln	Phe	Asn
	290					295					300				
Gln	Tyr	Lys	Thr	Glu	Ala	Ala	Ser	Arg	Tyr	Asn	Leu	Thr	Ile	Ser	Asp
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Val	Ser	Val	Ser	Asp	Val	Pro	Phe	Pro	Phe	Ser	Ala	Gln	Ser	Gly	Ala
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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&lt;210&gt; 17

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

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Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
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His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
20           25           30

Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
35           40           45

Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
50           55           60

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Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp  
65 70 75 80

Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met  
85 90 95

Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile  
100 105 110

Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg  
115 120 125

Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr  
130 135 140

Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser  
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Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly  
165 170 175

<210> 18  
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<212> DNA  
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Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro  
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Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly  
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<210> 20

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<212> DNA

<213> Homo sapiens

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<210> 21

<211> 50

<212> PRT

<213> Homo sapiens

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 20 25 30

Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro  
 35 40 45

Phe Pro  
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<210> 22

<211> 150

<212> DNA

<213> Homo sapiens

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gacgtcagcg tgagtgatgt gccatttcct

150

&lt;210&gt; 23

&lt;211&gt; 49

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 23

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Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala  
 35 40 45

Gly

&lt;210&gt; 24

&lt;211&gt; 147

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 24

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cctttctctg cccagtctgg ggctggg 147

&lt;210&gt; 25

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

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 20 25 30

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln  
 35 40 45

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val  
 50 55 60

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His  
65 70 75 80

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg  
85 90 95

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro  
100 105 110

Phe Ser Ala Gln Ser Gly Ala Gly  
115 120

<210> 26  
<211> 360  
<212> DNA  
<213> Homo sapiens

<400> 26  
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atgtttttgc agatttataa acaaggggggt tttctgggcc tctccaatat taagttcagg 180  
ccaggatctg tgggtgtaca attgactctg gccttccgag aaggtaccat caatgtccac 240  
gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 300  
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<210> 27  
<211> 77  
<212> PRT  
<213> Homo sapiens

<400> 27

Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg Glu Thr Phe Leu Lys  
1 5 10 15

Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly  
20 25 30

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr  
35 40 45

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser  
50 55 60

Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly



65

70

75

<210> 28  
 <211> 231  
 <212> DNA  
 <213> Homo sapiens

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 acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac 180  
 gtcagcgtga gtgatgtgcc atttcctttc tctgcccagt ctggggctgg g 231

<210> 29  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 29

Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn  
 1 5 10 15

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 20 25 30

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln  
 35 40 45

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val  
 50 55 60

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His  
 65 70 75 80

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg  
 85 90 95

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro  
 100 105 110

<210> 30  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

<400> 30  
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 ccaggatctg tgggtgtaca attgactctg gccttccgag aaggtaccat caatgtccac 240  
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 atctcagacg tcagcgtgag tgatgtgcca tttcct 336

<210> 31  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens

<400> 31

Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg Glu Thr Phe Leu Lys  
 1 5 10 15

Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly  
 20 25 30

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr  
 35 40 45

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser  
 50 55 60

Asp Val  
 65

<210> 32  
 <211> 198  
 <212> DNA  
 <213> Homo sapiens

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 gtcagcgtga gtgatgtg 198

<210> 33  
 <211> 232  
 <212> PRT  
 <213> HS

<400> 33

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1	5	10	15
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro	20	25	30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val	35	40	45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val	50	55	60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln	65	70	75
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln	85	90	95
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala	100	105	110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro	115	120	125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr	130	135	140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser	145	150	155
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr	165	170	175
Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe Leu Tyr	180	185	190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe	195	200	205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys	210	215	220
Ser Leu Ser Leu Ser Pro Gly Lys	225	230	
<210> 34			
<211> 699			

&lt;212&gt; DNA

&lt;213&gt; HS

&lt;400&gt; 34

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acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc      360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc      480
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cccgtgctgg actccgtcgg ctcttcttct ctctacagca agctcaccgt ggacaagagc      600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      660
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&lt;210&gt; 35

&lt;211&gt; 230

&lt;212&gt; PRT

&lt;213&gt; HS

&lt;400&gt; 35

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Lys Ser Cys Asp Lys Pro His Thr Cys Pro Leu Cys Pro Ala Pro Glu
1           5           10           15

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
20           25           30

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
35           40           45

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
50           55           60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
65           70           75           80

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
85           90           95

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro

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100	105	110
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu		
115	120	125
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn		
130	135	140
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile		
145	150	155
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Ala		
165	170	175
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys		
180	185	190
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys		
195	200	205
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu		
210	215	220
Ser Leu Ser Pro Gly Lys		
225	230	

<210> 36  
 <211> 690  
 <212> DNA  
 <213> HS

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 gaggtcacat gcgtggtagt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 180  
 tacgtggagc gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 240  
 agcacgtacc gtgtggtagt cgtcctcacc gtctgcacc aggactggct gaatggcaag 300  
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 360  
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggatgag 420  
 ctgaccaaga accaggtcag cctgacctgc ctagtcaaag gcttctatcc cagcgacatc 480  
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaaggccac gcctcccgtg 540  
 ctggactccg acggtctctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 600

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacag 660

cagaagagcc tctccctgtc tccgggtaaa 690

<210> 37

<211> 228

<212> PRT

<213> HS

<400> 37

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val  
1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu  
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr  
65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn  
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro  
100 105 110

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln  
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

195

200

205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 210 215 220

Ser Pro Gly Lys  
 225

<210> 38  
 <211> 687  
 <212> DNA  
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 gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 240  
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 aagtgaagg tctccaacaa aggcctccca gccccatcg agaaaacat ctccaaaacc 360  
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 aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 480  
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 tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 600  
 gggaacgtct tctcatgctc cgtgatgcat gaggtctctgc acaaccacta cacacagaag 660  
 agcctctccc tgtctccggg taaatga 687

<210> 39  
 <211> 229  
 <212> PRT  
 <213> Homo Sapiens

<400> 39

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe  
 1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr  
 20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val  
 35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val  
 50 55 60  
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser  
 65 70 75 80  
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
 85 90 95  
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser  
 100 105 110  
 Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro  
 115 120 125  
 Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln  
 130 135 140  
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala  
 145 150 155 160  
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
 165 170 175  
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu  
 180 185 190  
 Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser  
 195 200 205  
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser  
 210 215 220  
 Leu Ser Leu Gly Lys  
 225

<210> 40  
 <211> 690  
 <212> DNA  
 <213> HS

<400> 40  
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acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgar cggcaaggag      300
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accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc      480
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg      540
gactccgacg gctccttctt cctctacagc aggctaaccg tggacaagag cagktggcag      600
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<210> 41  
 <211> 585  
 <212> PRT  
 <213> HS

<400> 41

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu  
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Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln  
 20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Gln Leu Leu Phe Phe Ala Lys Arg  
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys  
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp  
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser  
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His  
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser  
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala  
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg  
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr  
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Pro Asp Pro His Glu  
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Met Glu Glu Pro  
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Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

<210>	42
<211>	1758
<212>	DNA
<213>	HS

27/36

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cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300
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gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaa atacttatat 420
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gctgccttag gcttataa 1758

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<210> 43
<211> 110
<212> PRT
<213> Homo Sapiens

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&lt;400&gt; 43

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 1 5 10 15

Val Cys Ala Tyr Asp Pro Glu Ala Ala Ser Ala Pro Gly Ser Gly Asn  
 20 25 30

Pro Cys His Glu Ala Ser Ala Ala Gln Lys Glu Asn Ala Gly Glu Asp  
 35 40 45

Pro Gly Leu Ala Arg Gln Ala Pro Lys Pro Arg Lys Gln Arg Ser Ser  
 50 55 60

Leu Leu Glu Lys Gly Leu Asp Gly Ala Lys Lys Ala Val Gly Gly Leu  
 65 70 75 80

Gly Lys Leu Gly Lys Asp Ala Val Glu Asp Leu Glu Ser Val Gly Lys  
 85 90 95

Gly Ala Val His Asp Val Lys Asp Val Leu Asp Ser Val Leu  
 100 105 110

&lt;210&gt; 44

&lt;211&gt; 333

&lt;212&gt; DNA

&lt;213&gt; HS

&lt;400&gt; 44

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 gatccagagg ccgcctctgc cccaggatcg ggggaaccctt gccatgaagc atcagcagct 120  
 caaaaggaaa atgcaggtga agaccagggg ttagccagac aggcaccaa gccaaggaag 180  
 cagagatcca gccttctgga aaaaggccta gacggagcaa aaaaagctgt ggggggactc 240  
 ggaaaaactag gaaaagatgc agtcgaagat ctagaaagcg tgggtaaagg agccgtccat 300  
 gacgttaaag acgtccttga ctcagtacta tag 333

&lt;210&gt; 45

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Synthesized Sequence

&lt;400&gt; 45

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21

<210> 46  
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<212> DNA  
<213> Artificial

<220>  
<223> Synthesized Sequence

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<210> 47  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Synthesized Sequence

<400> 47  
aaaaggaaaa tgcaggtgaa g 21

<210> 48  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Synthesized Sequence

<400> 48  
aaaggaaaat gcaggtgaag a 21

<210> 49  
<211> 21  
<212> DNA  
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<220>  
<223> Synthesized Sequence

<400> 49  
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<210> 50  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Sythesized Sequence

<400> 50  
aaaatgcagg tgaagaccca g 21

<210> 51  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Synthesized sequence

<400> 51  
aaatgcaggt gaagacccag g 21

<210> 52  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Synthesized Sequence

<400> 52  
aaagccaagg aagcagagat c 21

<210> 53  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Synthesized Sequence

<400> 53  
aagccaagga agcagagatc c 21

<210> 54  
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<212> DNA  
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<220>  
<223> Synthesized Sequence

<400> 54  
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<210> 55  
<211> 21  
<212> DNA  
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<220>  
<223> Synthesized Sequence

<400> 55  
aagcagagat ccagccttct g 21

<210> 56

<211> 21  
<212> DNA  
<213> Artificial

<220>  
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 35 40 45  
 Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val  
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 Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn  
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 85 90 95  
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Gln Pro Glu Asn Asn Tyr Lys Ala Thr Pro Pro Val Leu Asp Ser Asp  
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Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
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